M. Wilson

1633

ENTERED

```
       RAW SEQUENCE LISTING              DATE: 05/04/2000
       PATENT APPLICATION:  US/08/900,220B     TIME: 13:10:49

       Input Set : A:\ONV-044.01.txt
       Output Set: C:\CRF3\REFHOLD\05042000\H900220B.raw
```

```
      4 (1) GENERAL INFORMATION:
C--> 6      (i) APPLICANT: Miao, Ningning
      7                    Wang, Monica
      8                    Mahanthappa, Nagesh K.
      9                    Jin, Ping
     10                    Wang Pang, Kevin
     12     (ii) TITLE OF INVENTION: Method of Treating Dopaminergic and
     13                    GABA-nergic Disorders
     15   (iii) NUMBER OF SEQUENCES: 22
     17    (iv) CORRESPONDENCE ADDRESS:
     18          (A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP
     19          (B) STREET: ONE POST OFFICE SQUARE
     20          (C) CITY: Boston
     21          (D) STATE: MA
     22          (E) COUNTRY: USA
     23          (F) ZIP: 02109
     25     (v) COMPUTER READABLE FORM:
     26          (A) MEDIUM TYPE: Floppy disk
     27          (B) COMPUTER: IBM PC compatible
     28          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     29          (D) SOFTWARE: AscII (text)
C--> 31    (vi) CURRENT APPLICATION DATA:
C--> 32          (A) APPLICATION NUMBER: US/08/900,220B
C--> 33          (B) FILING DATE: 24-Jul-1997
     34          (C) CLASSIFICATION:
     36   (viii) ATTORNEY/AGENT INFORMATION:
     37          (A) NAME: Vincent, Matthew P.
     38          (B) REGISTRATION NUMBER: 36,709
     39          (C) REFERENCE/DOCKET NUMBER: ONV-044.01
     41    (ix) TELECOMMUNICATION INFORMATION:
     42          (A) TELEPHONE: (617) 832-1000
     43          (B) TELEFAX: (617) 832-7000
     46 (2) INFORMATION FOR SEQ ID NO: 1:
     47     (i) SEQUENCE CHARACTERISTICS:
     48          (A) LENGTH: 1277 base pairs
     49          (B) TYPE: nucleic acid
     50          (C) STRANDEDNESS: both
     51          (D) TOPOLOGY: linear
     53    (ii) MOLECULE TYPE: cDNA
     55    (ix) FEATURE:
     56          (A) NAME/KEY: CDS
     57          (B) LOCATION: 1..1275
     59    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     61 ATG GTC GAA ATG CTG CTG TTG ACA AGA ATT CTC TTG GTG GGC TTC ATC      48
     62 Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
     63  1           5                   10                  15
     65 TGC GCT CTT TTA GTC TCC TCT GGG CTG ACT TGT GGA CCA GGC AGG GGC      96
```

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RAW SEQUENCE LISTING                          DATE: 05/04/2000
PATENT APPLICATION:  US/08/900,220B           TIME: 13:10:49

        Input Set : A:\ONV-044.01.txt
        Output Set: C:\CRF3\REFHOLD\05042000\H900220B.raw
```

```
66 Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
67              20              25              30
69 ATT GGA AAA AGG AGG CAC CCC AAA AAG CTG ACC CCG TTA GCC TAT AAG    144
70 Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
71          35              40              45
73 CAG TTT ATT CCC AAT GTG GCA GAG AAG ACC CTA GGG GCC AGT GGA AGA    192
74 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
75      50              55              60
77 TAT GAA GGG AAG ATC ACA AGA AAC TCC GAG AGA TTT AAA GAA CTA ACC    240
78 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
79 65              70              75              80
81 CCA AAT TAC AAC CCT GAC ATT ATT TTT AAG GAT GAA GAG AAC ACG GGA    288
82 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
83              85              90              95
85 GCT GAC AGA CTG ATG ACT CAG CGC TGC AAG GAC AAG CTG AAT GCC CTG    336
86 Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
87          100             105             110
89 GCG ATC TCG GTG ATG AAC CAG TGG CCC GGG GTG AAG CTG CGG GTG ACC    384
90 Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
91          115             120             125
93 GAG GGC TGG GAC GAG GAT GGC CAT CAC TCC GAG GAA TCG CTG CAC TAC    432
94 Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
95      130             135             140
97 GAG GGT CGC GCC GTG GAC ATC ACC ACG TCG GAT CGG GAC CGC AGC AAG    480
98 Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys
99 145             150             155             160
101 TAC GGA ATG CTG GCC CGC CTC GCC GTC GAG GCC GGC TTC GAC TGG GTC   528
102 Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
103             165             170             175
105 TAC TAC GAG TCC AAG GCG CAC ATC CAC TGC TCC GTC AAA GCA GAA AAC   576
106 Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
107             180             185             190
109 TCA GTG GCA GCG AAA TCA GGA GGC TGC TTC CCT GGC TCA GCC ACA GTG   624
110 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
111         195             200             205
113 CAC CTG GAG CAT GGA GGC ACC AAG CTG GTG AAG GAC CTG AGC CCT GGG   672
114 His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
115     210             215             220
117 GAC CGC GTG CTG GCT GCT GAC GCG GAC GGC CGG CTG CTC TAC AGT GAC   720
118 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
119 225             230             235             240
121 TTC CTC ACC TTC CTC GAC CGG ATG GAC AGC TCC CGA AAG CTC TTC TAC   768
122 Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
123             245             250             255
125 GTC ATC GAG ACG CGG CAG CCC CGG GCC CGG CTG CTA CTG ACG GCG GCC   816
126 Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala
127         260             265             270
129 CAC CTG CTC TTT GTG GCC CCC CAG CAC AAC CAG TCG GAG GCC ACA GGG   864
130 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
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RAW SEQUENCE LISTING                    DATE: 05/04/2000
PATENT APPLICATION:  US/08/900,220B         TIME: 13:10:49

Input Set : A:\ONV-044.01.txt
Output Set: C:\CRF3\REFHOLD\05042000\H900220B.raw

131          275                   280                   285
133 TCC ACC AGT GGC CAG GCG CTC TTC GCC AGC AAC GTG AAG CCT GGC CAA          912
134 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
135          290                   295                   300
137 CGT GTC TAT GTG CTG GGC GAG GGC GGG CAG CAG CTG CTG CCG GCG TCT          960
138 Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser
139 305                   310                   315.                  320
141 GTC CAC AGC GTC TCA TTG CGG GAG GAG GCG TCC GGA GCC TAC GCC CCA          1008
142 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
143          325                   330                   335
145 CTC ACC GCC CAG GGC ACC ATC CTC ATC AAC CGG GTG TTG GCC TCC TGC          1056
146 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
147          340                   345                   350
149 TAC GCC GTC ATC GAG GAG CAC AGT TGG GCC CAT TGG GCC TTC GCA CCA          1104
150 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
151          355                   360                   365
153 TTC CGC TTG GCT CAG GGG CTG CTG GCC GCC CTC TGC CCA GAT GGG GCC          1152
154 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
155          370                   375                   380
157 ATC CCT ACT GCC GCC ACC ACC ACC ACT GGC ATC CAT TGG TAC TCA CGG          1200
158 Ile Pro Thr Ala Ala Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
159 385                   390                   395                   400
160 CTC CTC TAC CGC ATC GGC AGC TGG GTG CTG GAT GGT GAC GCG CTG CAT          1248
161 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
162          405                   410                   415
164 CCG CTG GGC ATG GTG GCA CCG GCC AGC TG                                   1277
165 Pro Leu Gly Met Val Ala Pro Ala Ser
166          420                   425
169 (2) INFORMATION FOR SEQ ID NO: 2:
171     (i) SEQUENCE CHARACTERISTICS:
172          (A) LENGTH: 1190 base pairs
173          (B) TYPE: nucleic acid
174          (C) STRANDEDNESS: both
175          (D) TOPOLOGY: linear
177     (ii) MOLECULE TYPE: cDNA
179     (ix) FEATURE:
180          (A) NAME/KEY: CDS
181          (B) LOCATION: 1..1191
183     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
185 ATG GCT CTG CCG GCC AGT CTG TTG CCC CTG TGC TGC TTG GCA CTC TTG           48
186 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
187 1                 5                   10                  15
189 GCA CTA TCT GCC CAG AGC TGC GGG CCG GGC CGA GGA CCG GTT GGC CGG           96
190 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
191          20                   25                   30
193 CGG CGT TAT GTG CGC AAG CAA CTT GTG CCT CTG CTA TAC AAG CAG TTT          144
194 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
195          35                   40                   45
197 GTG CCC AGT ATG CCC GAG CGG ACC CTG GGC GCG AGT GGG CCA GCG GAG          192
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RAW SEQUENCE LISTING         DATE: 05/04/2000
PATENT APPLICATION:  US/08/900,220B     TIME: 13:10:49

Input Set : A:\ONV-044.01.txt
Output Set: C:\CRF3\REFHOLD\05042000\H900220B.raw

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198 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
199     50              55                  60
201 GGG AGG GTA ACA AGG GGG TCG GAG CGC TTC CGG GAC CTC GTA CCC AAC      240
202 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
203 65              70                  75                  80
205 TAC AAC CCC GAC ATA ATC TTC AAG GAT GAG GAG AAC AGC GGC GCA GAC      288
206 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
207             85                  90                  95
209 CGC CTG ATG ACA GAG CGT TGC AAA GAG CGG GTG AAC GCT CTA GCC ATC      336
210 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
211         100                 105                 110
213 GCG GTG ATG AAC ATG TGG CCC GGA GTA CGC CTA CGT GTG ACT GAA GGC      384
214 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
215         115                 120                 125
217 TGG GAC GAG GAC GGC CAC CAC GCA CAG GAT TCA CTC CAC TAC GAA GGC      432
218 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
219     130                 135                 140
221 CGT GCC TTG GAC ATC ACC ACG TCT GAC CGT GAC CGT AAT AAG TAT GGT      480
222 Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
223 145                 150                 155                 160
225 TTG TTG GCG CGC CTA GCT GTG GAA GCC GGA TTC GAC TGG GTC TAC TAC      528
226 Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
227                 165                 170                 175
229 GAG TCC CGC AAC CAC ATC CAC GTA TCG GTC AAA GCT GAT AAC TCA CTG      576
230 Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
231             180                 185                 190
233 GCG GTC CGA GCC GGA GGC TGC TTT CCG GGA AAT GCC ACG GTG CGC TTG      624
234 Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
235         195                 200                 205
237 CGG AGC GGC GAA CGG AAG GGG CTG AGG GAA CTA CAT CGT GGT GAC TGG      672
238 Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
239 210                 215                 220
241 GTA CTG GCC GCT GAT GCA GCG GGC CGA GTG GTA CCC ACG CCA GTG CTG      720
242 Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu
243 225                 230                 235                 240
245 CTC TTC CTG GAC CGG GAT CTG CAG CGC CGC GCC TCG TTC GTG GCT GTG      768
246 Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
247                 245                 250                 255
249 GAG ACC GAG CGG CCT CCG CGC AAA CTG TTG CTC ACA CCC TGG CAT CTG      816
250 Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
251             260                 265                 270
253 GTG TTC GCT GCT CGC GGG CCA GCG CCT GCT CCA GGT GAC TTT GCA CCG      864
254 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
255         275                 280                 285
257 GTG TTC GCG CGC CGC TTA CGT GCT GGC GAC TCG GTG CTG GCT CCC GGC      912
258 Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
259     290                 295                 300
261 GGG GAC GCG CTC CAG CCG GCG CGC GTA GCC CGC GTG GCG CGC GAG GAA      960
262 Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
```

```
        RAW SEQUENCE LISTING              DATE: 05/04/2000
        PATENT APPLICATION:  US/08/900,220B      TIME: 13:10:49

        Input Set : A:\ONV-044.01.txt
        Output Set: C:\CRF3\REFHOLD\05042000\H900220B.raw

263 305                 310                 315                 320
265 GCC GTG GGC GTG TTC GCA CCG CTC ACT GCG CAC GGG ACG CTG CTG GTC      1008
266 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
267                 325                 330                 335
269 AAC GAC GTC CTC GCC TCC TGC TAC GCG GTT CTA GAG AGT CAC CAG TGG      1056
270 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
271                 340                 345                 350
273 GCC CAC CGC GCC TTC GCC CCT TTG CGG CTG CTG CAC GCG CTC GGG GCT      1104
274 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
275                 355                 360                 365
277 CTG CTC CCT GGG GGT GCA GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT      1152
278 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
279         370                 375                 380
281 CGC CTC CTT TAC CGC TTG GCC GAG GAG TTA ATG GGC TG                   1190
282 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
283 385                 390                 395
286 (2) INFORMATION FOR SEQ ID NO: 3:
288     (i) SEQUENCE CHARACTERISTICS:
289         (A) LENGTH: 1281 base pairs
290         (B) TYPE: nucleic acid
291         (C) STRANDEDNESS: both
292         (D) TOPOLOGY: linear
294     (ii) MOLECULE TYPE: cDNA
297     (ix) FEATURE:
298         (A) NAME/KEY: CDS
299         (B) LOCATION: 1..1233
301     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
303 ATG TCT CCC GCC TGG CTC CGG CCC CGA CTG CGG TTC TGT CTG TTC CTG        48
304 Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
305  1               5               10                  15
307 CTG CTG CTG CTT CTG GTG CCG GCG GCG CGG GGC TGC GGG CCG GGC CGG        96
308 Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
309             20                  25                  30
311 GTG GTG GGC AGC CGC CGG AGG CCG CCT CGC AAG CTC GTG CCT CTT GCC       144
312 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
313         35                  40                  45
315 TAC AAG CAG TTC AGC CCC AAC GTG CCG GAG AAG ACC CTG GGC GCC AGC       192
316 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
317     50                  55                  60
319 GGG CGC TAC GAA GGC AAG ATC GCG CGC AGC TCT GAG CGC TTC AAA GAG       240
320 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
321  65                  70                  75                  80
323 CTC ACC CCC AAC TAC AAT CCC GAC ATC ATC TTC AAG GAC GAG GAG AAC       288
324 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
325                 85                  90                  95
327 ACG GGT GCC GAC CGC CTC ATG ACC CAG CGC TGC AAG GAC CGT CTG AAC       336
328 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
329             100                 105                 110
331 TCA CTG GCC ATC TCT GTC ATG AAC CAG TGG CCT GGT GTG AAA CTG CGG       384
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VERIFICATION SUMMARY                    DATE: 05/04/2000
PATENT APPLICATION:   US/08/900,220B    TIME: 13:10:50

Input Set : A:\ONV-044.01.txt
Output Set: C:\CRF3\REFHOLD\05042000\H900220B.raw

L:6 M:220 C: Keyword misspelled, [(i) APPLICANT:]
L:792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1734 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2333 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22